If any fee is believed to be due in connection with this filing, please charge our Deposit Account No. 23-2825.

Respectfully submitted,

John R. Van Amsterdam, Reg. No. 40,212
Wolf, Greenfield & Sacks, P.C.
600 Atlantic Avenue
Boston, MA 02210-2211
(617) 720-3500

Docket No. B00192/70019
Date: August 1, 2002

Page 22, line 23 through Page 23 line 20:

FIGURE 1 shows a sequence of nucleotides which is the left arm end-sequence of YAC 766_f_12; (SEQ ID NO: 1).

FIGURE 2 shows a sequence of nucleotides which is a right arm end-sequence of YAC 766_f_12; (SEQ ID NO: 2).

FIGURE 3 shows a sequence of nucleotides which is the left arm end-sequence of YAC 717_d_3; (SEQ ID NO:3).

FIGURE 4 shows a sequence of nucleotides which is the right arm end-sequence of YAC 717_d_3; (SEQ ID NO:4).

FIGURE 5 shows a sequence of nucleotides which is the right arm end-sequence of YAC 731_c_7; (SEQ ID NO:5).

FIGURE 6 shows a sequence of nucleotides which is the left arm end-sequence of YAC 752_g_8; (SEQ ID NO:6).

FIGURE 7 shows a sequence of nucleotides which is the left arm end-sequence of YAC 942_c_3; (SEQ ID NO:7).

FIGURE 8 shows a sequence of nucleotides which is the right arm end-sequence of YAC 942_c_3; (SEQ ID NO:8).

FIGURE 9 shows a sequence of nucleotides which is the left arm end-sequence of YAC 961_h_9; (SEQ ID NO:9).

FIGURE 10 shows a sequence of nucleotides which is the right arm end-sequence of YAC 961_h_9; (SEQ ID NO:10).

FIGURE 11 shows a sequence of nucleotides which is the left arm end-sequence of YAC 907_e_1; (SEQ ID NO:11).

Page 23, line 35 through page 24, line 26:

FIGURE 15 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 961_h_9 (SEQ ID NO:12). The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence (SEQ ID NOs:13 and 14).

FIGURE 16 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 766_f_12 (SEQ ID NO: 15). The sequence is italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence (SEQ ID NOs:16 and 17).

FIGURE 17 shows (a) a CAG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 766_f_12 (SEQ ID NO: 18). The sequence is italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence (SEQ ID NOs: 19 and 20).

FIGURE 18 shows (a) a CTG repeat (in bold) and surrounding nucleotide sequence isolated from YAC 907_e_1 (SEQ ID NO: 21). The sequence in italics is derived from End Rescue of the fragmented YAC. (b) PCR primers that can be used to determine the extent of trinucleotide repeats in the sequence (SEQ ID NOs:22 and 23).

Page 36 line 1 through Page 61 line 22:

<u>D18S60:</u>

Database ID: AFM178XE3 (Also known as 178xe3, Z16781, D18S60)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
   Left = CCTGGCTCACCTGGCA (SEQ ID NO:24)
   Right = TTGTAGCATCGTTGTAATGTTCC (SEQ ID NO:25)
   Product Length = 157
   Review complete sequence:
AGCTAT<u>CCTGGCTCACCTGGCA</u>AAAATACAGTGTATACACACACACACACACAC
ACACACACACACAGAGTGTNTTANTNATTCCAGCAAATAATATTACATATAAAGA
TCTAATTGGTTCATCATGTAAATTTAGTA<u>GGAACATTACAACGATGCTACAA</u>GANTT
TATCCAAAACTGAGATTTCCTTAGAATATCTGTTAAAGTAATTTTATTCAGTTAATA
GAAATTCTATTGAAAACATCAAACTTATAAAGCT (SEQ ID NO:26)

Genbank ID: Z16781
Description: H. sapiens (D18S60) DNA segment containing (CA) repeat; clone
Search for GDB entry

<u>WI-9222:</u>

Database ID: UTR-03540 (Also known as G06101, D18S1033, 9222, X63657)
Source: WICGR: Primers derived from Genbank sequences
Chromosome: Chr18

Primers:
   Left = GATCCCATAAAGCTACGAGGG (SEQ ID NO:27)
   Right = GAGTCTAAAGACAAGAAAGCATTGC (SEQ ID NO:28)
   Product Length = 99
   Review complete sequence:
TCTTCTTACCCCTTGGAAGAAGACTGTTTCCAAATAATTTGAACAGCTTGCTGCTAA
ATGGGACCCAATTTTTGGCCTATAGACACTTATGTATTGTTTTCGAATACGTCAGATT
GGACCAGTGCTCTTCAGGAATGTGGCTGCAAGCAAGGGGCTAGAAGTTCACCTCCT
GACAGTATTATTAATACTATGCAAATATGGAATAGGAGACCATTTGATTTTCTAGGC
TTTGTGGTAGAGAGGTGAAGGTATGAGAATTAATAGCGTGTGAACAAAGTAAAGAA
CAGGATTCCAGAATGATCATTAAATTTGTTTCTATTTATTCTTTTTTGCCCCCCTAGA
GATTAAGTCCAGAAATGTACTTTCTGGCACATAAAGAAATCTTGAGGACTTTGTTTA
AACCTTCCATAAAAAAACAATTTTCGGTTTCTCGGGTNNNNNNNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTTCTTTCTTTG
TGTATTTTATTCAAGATGAGTTGGACCCATTGCCAGTGAGTCTGAATGTCACTGACA
GCCCTGTGTTGTGCTCAGGACTCACTCTGCTGCTGGTGGAAACTCATGGCTTCTCTCT
CTCTTT<u>GATCCCATAAAGCTACGAGGG</u>GACGGGAGAGGGCAGTGCAATGGGAAGT
AAAGAGATATTTTCCAGTAGGAAAA<u>GCAATGCTTTCTTGTCTTTAGACTC</u>AAATGCT
TAGGGAACGTTTCATTTCTCATTCATGGGGAAAGGCAGCCTCCTTAAATGTTTTCTG
AAGAGCGGTAAAATCTAGAAGCTTAAGAATTTACAGTTCCTTCAATAACCATGATGA
CCTGAAGTTCACCTATCCCATTTTAGCATCTACTTGTTTTTCCCATCTCTTCCTTTCCA

ATTTTGCTTATACTGCTGTAATATTTTTGTNNNNNNNNNNNNNNNNNNNNNNNNNNNG
ACCAGCTAAAATTTTCGACTTGACTTTTTAACTTAACTCATGAATTAATTAAAGCAA
ATGAAAAAATTAAAAAGTGTGACTTTTTCTCGGAGCATATATGTAGCTTTTAGGAAA
GGCTGATGATGGTATAAAGTTTGCTCATTAAGAAAAAAAGACAAGGCTGATTTTGA
AGAGAGTTGCTTTTGAAATAAAATGATCA (SEQ ID NO:29)

Genbank ID: X63657
Description: H.sapiens fvt1 mRNA
Search for GDB entry

WI-7336:

Database ID: UTR-04664 (Also known as PI5, G00-679-135, G06527, 7336, U04313)
Source: WICGR: Primers derived from Genbank sequences
Chromosome: Chr18

Primers:
    Left = AGACATTCTCGCTTCCCTGA (SEQ ID NO:30)
    Right = AATTTTGACCCCTTATGGGC (SEQ ID NO:31)
    Product Length = 332
    Review complete sequence:

TAAGTGGCATAGCCCATGTTAAGTCCTCCCTGACTTTTCTGTGGATGCCGATTTCTGT
AAACTCTGCATCCAGAGATTCATTTTCTAGATACAATAAATTGCTAATGTTGCTGGA
TCAGGAAGCCGCCAGTACTTGTCATATGTAGCCTTCACACAGATAGACCNNNNNNN
NNNNCCAATTCTATCTTTTGTTTCCTTTTTTCCCATAAGACAATGACATACGCTTTTA
ATGAAAAGGAATCACGTTAGAGGAAAAATATTTATTCATTATTTGTCAAATTGTCCG
GGGTAGTTGGCAGAAATACAGTCTTCCACAAAGAAAATTCCTATAAGGAAGATTTG
GAAGCTCTTCTTCCCAGCACTATGCTTTCCTTCTTTGGGATAGAGAATGTTCC<u>AGACA
TTCTCGCTTCCCTGA</u>AAGACTGAAGAAAGTGTAGTGCATGGGACCCACGAAACTGCC
CTGGCTCCAGTGAAACTTGGGCACATGCTCAGGCTACTATAGGTCCAGAAGTCCTTA
TGTTAAGCCCTGGCAGGCAGGTGTTTATTAAAATTCTGAATTTTGGGGATTTTCAAA
AGATAATATTTTACATACACTGTATGTTATAGAACTTCATGGATCAGATCTGGGGCA
GCAACCTATAAATCAACACCTTAATATGCTGCAACAAATGTAGAATATTCAGACA
AAATGGATACATAAAGACTAAGTA<u>GCCCATAAGGGGTCAAAA</u>TTTGCTGCCAAATG
CGTATGCCACCAACTTACAAAAACACTTCGTTCGCAGAGCTTTTCAGATTGTGGAAT
GTTGGATAAGGAATTATAGACCTCTAGTAGCTGAAATGCAAGACCCCAAGAGGAAG
TTCAGATCTTAATATAAATTCACTTTCATTTTGATAGCTGTCCCATCTGGTCATGTG
GTTGGCACTAGACTGGTGGCAGGGGCTTCTAGCTGACTCGCACAGGGATTCTCACAA
TAGCCGATATCAGAATTTGTGTTGAAGGAACTTGTCTCTTCATCTAATATGATAGCG
GGAAAAGGAGAGGAAACTACTGCCTTTAGAAAATATAAGTAAAGTGATTAAAGTGC
TCACGTTACCTTGACACATAGTTTTTCAGTCTATGGGTTTAGTTACTTTAGATGGCAA
GCATGTAACTTATATTAATAGTAATTTGTAAAGTTGGGTGGATAAGCTATCCCTGTT
GCCGGTTCATGGATTACTTCTCTATAAAAAATATATATTTACCAAAAAATTTTGTGA
CATTCCTTCTCCCATCTCTTCCTTGACATGCATTGTAAATAGGTTCTTCTTGTTCTGAG

ATTCAATATTGAATTTCTCCTATGCTATTGACAATAAAATATTATTGAACTACC (SEQ
ID NO:32)

Genbank ID: G06527
Description: WICGR: Random genome wide STSs
X
WI-8145:

Database ID: EST102441 (Also known as D18S1234, G00-677-827, G06845, 8145, T49159)
Source: WICGR: STSs derived from dbEST sequences
Chromosome: Chr18
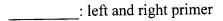
Primers:
    Left = GAAATGCACATAACATATATTTGCC (SEQ ID NO:33)
    Right = TGCTCACTGCCTATTTAATGTAGC (SEQ ID NO:34)
    Product Length = 184
    Review complete sequence:

GTTGTTTGGANGCAGGTTTATTTATTATATACTTGCAATTGAATATAAGATACAGAC
ATATATATGTGTTATGTATTTCTAGAAATGCACATAACATATATTTGCCTATTGTTTA
ATGTTTTTTCCAGANATTTATTACAGAAGGGCATGGAGGGATACCTACTTATTCTTC
ATTATGAGAACAATTAAAGGCATTTATTAGATAGGAAATTAACAGANCATCTGCTTC
TATAACTTTATTAGCTACATTAAATAGGCAGTGAGCANTAATTTAAAANCTCACCAT
TATATAAANTANTAAATACCAAAGTAAAAG (SEQ ID NO:35)

_____ : left and right primer

PCR Conditions

Genbank ID: T49159
Description: yb09e07.s1 Homo sapiens cDNA clone 70692 3' similar to gb:J02685
UniGene Cluster Description: Human mRNA for Arg-Serpin (plasminogen activator-inhibitor 2,
PAI-2) Search for GDB entry

WI-7061:

Database ID: UTR-02902 (Also known as PAI2, G00-678-979, G06377, 7061, M18082)
Source: WICGR: Primers derived from Genbank sequences
Chromosome: Chr18

Primers:
    Left = TGCTCTTCTGAACAACTTCTGC (SEQ ID NO:36)
    Right = ATAGAAGGGCATGGAGGGAT (SEQ ID NO:37)
    Product Length = 338
    Review complete sequence:

AACTAAGCGTGCTGCTTCTGCAAAAGATTTTTGTAGATGAGCTGTGTGCCTCAGAAT
TGCTATTTCAAATTGCCAAAAATTTAGAGATGTTTTCTACATATTTCTGCTCTTCTGA
ACAACTTCTGCTACCCACTAAATAAAAACACAGAAATAATTAGACAATTGTCTATTA
TAACATGACAACCCTATTAATCATTTGGTCTTCTAAAATGGGATCATGCCCATTTAG
ATTTTCCTTACTATCAGTTTATTTTTATAACATTAACTTTTACTTTGTTATTTATTATTT
TATATAATGGTGAGTTTTAAATTATTGCTCACTGCCTATTTAATGTAGCTAATAAAGT
TATAGAAGCAGATGATCTGTTAATTTCCTATCTAATAAATGCCTTTAATTGTTCTCAT
AATGAAGAATAAGTAGGTATCCCTCCATGCCCTTCTATAATAAATATCTGGAAAAAA
CATTAAACAATAGGCAAATATATGTTATGTGCATTTCTAGAAATACATAACACATAT
ATATGTCTGTATCTTATATTCAATTGCAAGTATATAATAAATAAACCTGCTTCCAAAC
AACNNNNNNNNNNNNNNNGGAATTC (SEQ ID NO:38)

PCR Conditions

Genbank ID: G06377
Description: WICGR: Random genome wide STSs

D18S68:

Database ID: AFM248YB9 (Also known as 248yb9, Z17122, D18S68)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = ATGGGAGACGTAATACACCC (SEQ ID NO:39)
    Right = ATGCTGCTGGTCTGAGG (SEQ ID NO:40)
    Product Length = 285
    Review complete sequence:

AAAGAGTTGGGGGTTGTGAATTCCCACACCAGTCAACTATTGGCTATGGGCTTACCAT
GGGAGACGTAATACACCCGGNACTTCCAACTCACATACCAGAGACATGGCTCTAGC
ACCCAATGGAAATATGCTGAATGTTGCAGGTGCAAGACAGCAACAAAGCAGACAGA
GGCACATAGACAAGGCACCAACAGTGTCCACTATACCCTGACAGTGTGGAAAGTTG
TAGATAGGATGAAGAGAAAGAATACACACACACACACACACACACACACACACAC
ACACACACACACACGGTAGANACTTACTACNCAAAGTGTGANCCTCAGACCAGC
AGCATCTGGCNAAATGGTGATCTATCACCTTCCAG (SEQ ID NO:41)

Genbank ID: Z17122
Description: H. sapiens (D18S68) DNA segment containing (CA) repeat; clone
WI-3170:

Database ID: MR3726 (Also known as D18S1037, G04207, HALd22f2, 3170)
Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:
   Left = TGTGCTACTGATTAAGGTAAAGGC (SEQ ID NO:42)
   Right = TGCTTCTTCAATTTGTAGAGTTGG (SEQ ID NO:43)
   Product Length = 156
   Review complete sequence

CTGAGACAAGGCAGGCAAACAACCTCTAAAAATCTACAATTGGTGATTGG<u>TGTGCT</u>
<u>ACTGATTAAGGTAAAGGC</u>ACAGAATTATACATCCAGGTTNCTATTACTTATGGCAGA
CTCAGGACCCAGGTTNAGAGACCACTGGCCTTAAGAAAAAAATGGGGTTCCTGAT
TTCTGGATAATAAT<u>CCAACTCTACAAATTGAAGAAGCA</u>ACATACCCTCTTTGTTA
(SEQ ID NO:44)

Genbank ID: G04207
Description: WICGR: Random genome wide STSs

<u>WI-5654:</u>

Database ID: MR10908 (Also known as D18S1259, G00-678-695, G05278, 5654)
Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:
   Left = CTTAATGAAAACAATGCCAGAGC (SEQ ID NO:45)
   Right = TGCAAAATGTGGAATAATCTGG (SEQ ID NO:46) ,
   Product Length = 149
   Review complete sequence:

CTACAAAATGCATGTGGCTTTGGCTTTGAAATAGTACACCCTATCAAAGACTAAATT
TT<u>CTTAATGAAAACAATGCCAGAGC</u>TTTTTTCATGATATTTGTTTTTAGAGATGGGG
AACAATCTGGACGTTGTTTCCTTATCTGGGTGGTAATCGAGGCTTAGCAATTTCCCA
CAGCGTTACACAAAT<u>CCAGATTATTCCACATTTGCA</u>AATA (SEQ ID NO:47)

Genbank ID: G05278
Description: WICGR: Random genome wide STSs

<u>D18S55:</u>

Database ID: AFM122XC1 (Also known as 122xc1, Z16621, D18S55, GC378-D18S55)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18
Primers:
   Left = GGGAAGTCAAATGCAAAATC (SEQ ID NO:48)
   Right = AGCTTCTGAGTAATCTTATGCTGTG (SEQ ID NO:49)

Product Length = 143
Review complete sequence:
AGCTGAACATGCCTTTTCATGGAGCAGTTTCNAAATACACTTTTGGTACAATCTGCA
GGTGGATATTTGGAGCTCAGGAGTTTGAGACCAGCCTGGGCAACATGGTGAAATCC
CGTCTCTACTAAAATACAAAAAATTAGCCAGGTGTGGCGGCATGTGCCTGTAGNCCC
AGGATGGATTGAGTGGGTGAGATATGGAATAAGTGGTGGGAAGTCAAATGCAAAAT
CAATTCAGTTTGTCAATATTGATTCTCTATTCTAGCCTGGCGTGGTTTTCCTCGTCA
CACACACACACACACACACACACACACACACACACACACACCACAGCATAAGATT
ACTCAGAAGCT (SEQ ID NO:50)

Genbank ID: Z16621
Description: H. sapiens (D18S55) DNA segment containing (CA) repeat; clone

D18S969:

Database ID: GATA-P18099 (Also known as G08003, CHLC.GATA69F01,
CHLC.GATA69F01.P18099)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
    Left = AACAAGTGTGTATGGGGGTG (SEQ ID NO:51)
    Right = CATATTCACCCAGTTTGTTGC (SEQ ID NO:52)
    Product Length = 365
    Review complete sequence:

CAGGGAAATGCAAATCAAAACCACAATGAGTTATCTCCTCATACCTTTAATGATGGC
TAATATTAAACAAGAGATAACAAGTGTGTATGGGGGTGTGGAGAAAAGAGAATGTN
CGAACACTCTTGGTTGAAATATAAGTTGGTAGANCCATTATGCAAAACAGTATGAAT
CTTTATCAGTATAANATTAGGACCTNGCATATGATCNCAGCAATCNCCACNTCTGNG
NGATCNCACNCNCTATCTCTCTATATCTATCTATCTATCTATCTATCTATCTATCTATC
TATCTATCTATCTATCTATCTGTCTGTCTATCATCTATCTATCTTCTATCTATCTATCT
ATCTTTCTATCTATCTATCTGTCTATCTATNCCGGAATATTTTTCAGCCATNNAAATA
AGGAAGTCCTGCTATTTGCAACAAACTGGGTGAATATGGAGAACGTTATGCTAAAT
GCAATATGCTAAAGACAGACACAGAAGACAAGTATGACCTCACTTATATGTGGAA
ACTGAAAAAGCCATACTCATTACAGCAAAGAGTAGAATGTTGGTTACCAGGGGCAA
AGAGGGTAGAAATGAGGGGAGTGAGAAAATGTCAATCAAAGTGTAAGAATGTTATA
ACATAAATAAATTCATAGAG (SEQ ID NO:53)

Genbank ID: G08003
Description: human STS CHLC.GATA69F01.P18099 clone GATA69F01.

D18S1113:

Database ID: AFM200VG9 (Also known as D18S1113, 200vg9, w2403)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs

Chromosome: Chr18

Primers:
  Left = GTTGACTCAAGTCCAAACCTG (SEQ ID NO:54)
  Right = CAAAGACATTGTAGACGTTCTCTG (SEQ ID NO:55)
  Product Length = 207
  Review complete sequence:
AGCTGCATATAAAACTATTCCATTTCACATTTTTGAAGACATTTGTAGCCATGATACT
TTGCTGTTGTCTGTGGGCCACCTCTTTTTGAAGTGTGTAGTTAACTGTGCTCCTGTAA
TCTGTTGTCTGTTGACTCAAGTCCAAACCTGTTCTGCGTGGCATGTTTCTNCAACTTG
ATGTGATGCTATTTATCACTTTCTTTGAAGTTAAGTCTCTATGTCTTTGTATTCTTTCT
GTGTACCCAGGGATATGTTTGTGCATGCACACGCATAAACACACACACACACAC
ACACACACAGAGACAGAGACAGAGAACGTCTACAATGTCTTTGTGAG (SEQ ID
NO:56)

D18S868:

Database ID: GATA-D18S868 (Also known as G09150, CHLC.GATA3E12,
CHLC.GATA3E12.496, CHLC.496, D18S868)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
  Left = AGCCAATACCTTGTAGTAAATATCC (SEQ ID NO:57)
  Right = GATTCTCCAGACAAATAATCCC (SEQ ID NO:58)
  Product Length = 189
  Review complete sequence:
GAGTGAGCCAATACCTTGTAGTAAATATCCATCTATCTTTGATGTATCTATGTATCTA
TCTTTGTATCTATATGTCTATGTATCTATGTATGTATGTATCTATCTATCATCTATCTA
TCTATCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCCNTTTGGG
ATTATTTGTCTGGAGAATCCTGATTAACATAGTCTGCTAACTTTTATCTGTATCTCCT
ATGTGTATGCTTCTCCTTCTTCCTGTCTCTCTCTCTTCTTTGTCCTCATTTAANCTCCTT
TCCTGGGNATATTGGNAATTTTGATTGGANTCTGGACANTGTAGGAGTAAAAATTT
(SEQ ID NO:59)

Genbank ID: G09150
Description: human STS CHLC.GATA3E12.P6553 clone GATA3E12.

WI-9959:

Database ID: MR12816 (Also known as D18S1251, G00-678-524, G05488, 9959)
Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:
    Left = TGCCAACAGCAGTCAAGC (SEQ ID NO:60)
    Right = AGCACCTGCAGCAGTAATAGC (SEQ ID NO:61)
    Product Length = 110
    Review complete sequence:
CtgttttatttgaaaaaaaaaatctgtctccaagaagaaaagttcattctACCTGTTGCCAACAGCAGTCAAGCGGA
CATGTTTAAAATTTTTTAAAAAAGTATTTTTTTTTCCAACTGGNGTTTAATAGCCTCA
TTTTGGCTTTTGCTATTACTGCTGCAGGTGCTTTNATTTTTTTCCTCTGCATTATAATT
AC (SEQ ID NO:62)

Genbank ID: G05488
Description: WICGR: Random genome wide STSs
Search for GDB entry

<u>D18S537:</u>

Database ID: CHLC.GATA2E06.13 (Also known as CHLC.13, GATA2E06, D18S537, GATA-
D18S537)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
    Left = TCCATCTATCTTTGATGTATCTATG (SEQ ID NO:63)
    Right = AGTTAGCAGACTATGTTAATCAGGA (SEQ ID NO:64)
    Product Length = 191
    Review complete sequence:
AAAGCTGAGTGAGCCAATACCTTGTAGTAAATATCCATCTATCTTTGATGTATCTAT
GTATCTATCTTTGTATCTATATGTCTATGTATCTATGTATGTATGTATCTATCTATCAT
CTATCTATCTATCATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATATCC
NTTNGGTATTATTNGTCTGGNGAATCCTGATTAACATAGTCTGCTAACTTNTATCTGT
ATCTNCTATGTGTATGCTTCTNCTTCTTCCTGTCTCTCTCTCTGCTTTGTCCTCAATTN
AAATCTCC (SEQ ID NO:65)

Genbank ID: G07990
Description: human STS CHLC.GATA2E06.P6006 clone GATA2E06.
Search for GDB entry

<u>D18S483:</u>

Database ID: AFM324WC9 (Also known as 324wc9, Z24399, D18S483)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = TTCTGCACAATTTCAATAGATTC (SEQ ID NO:66)

Right = GAACTGAGCAAACGAGTATGA (SEQ ID NO:67)
Product Length = 214
Review complete sequence:
AGCTCTGCTGGAAGAGCAGGGCTGTT<u>TTCTGCACAATTTCAATAGATT</u>CCCCTACCC
TGGGTTTTTCAGTAGATAGATAGATAGATGATAGATAGGTAGATAGATAGATAGAT
AGATAGATAGATAGATAGATAGATGATAGATAGATTTTATATATAGTATATAAAATC
TACACACACACACACACACACACACACATATTTGCCTTTCCTTGACTA<u>TCATACT
CGTTTGCTCAGTTC</u>TTTTTTTTTTTAAATTTTTGTTGTAAATCCAAAATGCTT (SEQ
ID NO:68)

Genbank ID: Z24399
Description: H. sapiens (D18S483) DNA segment containing (CA) repeat; clone
Search for GDB entry

D18S465:

Database ID: AFM260YH1 (Also known as 260yh1, Z23850, D18S465)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = ATATTCCCCTATGGAAGTACAG (SEQ ID NO:69)
    Right = AAAGTTAATTTTCAGGCACTCT (SEQ ID NO:70)
    Product Length = 232
    Review complete sequence:
AGCTCTGTCCCTCTAGAGAACGCTGACTAAT<u>ATATTCCCCTATGGAAGTACAG</u>ATGG
TTTTTNTAAAATAAATTTATCTGATTGTGATGAGATAATCATCATTTTTATGTTCAGT
GTTTTTCTAAATTTTTTATTGTTATTGTTTTTATACTCTAAATGGTTTTTAAATATGCA
CATATGTGCATATTTTACACACACACACACACACACACACTCTCTTTATTTAGAA
GCATTATAGAT<u>AGAGTGCCTGAAAATTAACTTTT</u>AACCNAAGAAAGACAATAAGG
AACAATAGGGAAGTTATCCTTTGCTAAGGGTATGGAAAATATTCACATATTATTTAT
AACANGTTAAACCAAGTCATGCTTGANTATAATAGCT (SEQ ID NO:71)

Genbank ID: Z23850
Description: H. sapiens (D18S465) DNA segment containing (CA) repeat; clone
Search for GDB entry

D18S968:

Database ID: GATA-P34272 (Also known as G10262, CHLC.GATA117C05,
CHLC.GATA117C05.P34272)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:

Left = GAAATTAACCAGACACTCCTAACC (SEQ ID NO:72)
Right = CTTAGAATTGCCTTTGCTGC (SEQ ID NO:73)
Product Length = 147
Review complete sequence:
GAATAAAAATATGAGGTATTAGAAATTTACAGATAGGAA<u>GAAATTAACCAGACACT
CCTAACC</u>ACCGATNAGTTTAAAGAGGAGATAGATAGATAGATGATAGATAGATAGA
TAGATAGATAGATACCACTGAAAATGCAANCACAAATTAGCAGATTATATGTGAT<u>G
CAGCAAAGGCAATTCTAAG</u>TAGATTCTAACTGCTACATTGATAGCAGTACCCACTGA
CATTACCGGAAAGGATGGTATCCATAACCACCTACCTATATACCTCCGCAGCTGGAN
ATTAGGNTTAAGCTTCTTNGGGCNCCTGGCGGCCCCNNTTGTGGTCCCCGGTNGGNC
CCCGNTTNNGNNTNGCTNNGNTTNCNTTGGNGNCCCCCNNTNGGTTTNNGGNNNNN
TNNNNNTNGNNNNNTTNCCCNNNNNNNNNTNTNNNNCNNNNNNNNNTNNNNNNNNN
NNNNGGNNNNNGGGN (SEQ ID NO:74)

Genbank ID: G10262
Description: human STS CHLC.GATA117C05.P34272 clone GATA117C05.

GATA-P6051:

Database ID: GATA-P6051 (Also known as CHLC.GATA3E08, CHLC.GATA3E08.P6051)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
    Left = GCAACAACCCTAATGAGTATACG (SEQ ID NO:75)
    Right = GAGTCTCACCAGGGCTTACA (SEQ ID NO:76)
    Product Length = 149
    Review complete sequence:
AAAGCTGTCTCCTTTTGTAAAGTGTGCTCAGAGGAATCTTTTTCAGTAAATAAAGTC
TGCACCCAGACATCTCACTTTGTATACCACGGAGAATTTACCATGACTCTTCTCAGT
GATAAACGTCAATATAGAATAATCAGGAGAAAAGAGAAATCCAGTAAAGAAATA
AGTCTGTAGAAA<u>GCAACAACCCTAATGAGTATACG</u>ATATCTATCTATCTATCTATCT
ATCTATCTATCTATCTATCTATGNATCTATCTATCTAACATTATATAAAATATA
TATTTCCTCCTGTATTGGGGCCCTGTG<u>TGTAAGCCCTGGTGAGACTC</u>AAAAATTTGA
NTATTCCTNTTTNT (SEQ ID NO:77)

Genbank ID: G09104
Description: human STS CHLC.GATA3E08.P6051 clone GATA3E08.

D18S875:

Database ID: GATA-D18S875 (Also known as G08001, CHLC.GATA52H04, D18S875)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
   Left = TCCTCTCATCTCGGATATGG (SEQ ID NO:78)
   Right = AAGGCTTTCAGACTTACACTGG (SEQ ID NO:79)
   Product Length = 394
   Review complete sequence:
TTATTTATTCACTCATTCAATAAATATTTATGAATTTCCTTTAATGGCNANGAAAGTA
TGTTTGGTACTGAATATGGTGAGCAAGATTTTCCTCTCATCTCGGATATGGAAAGAT
CTTGGAAATCATTATACNTCATACTTACAATANGAAAGAAGCTGAGCAATTTGAAA
ATCAACAATTTCTTTTGTACNTGTCAGAAAAGTGAAGATATATTAATCAGGGTTCTT
CAGAGAAACATAACCAATAGGNCACAGNTCTATATGNCCNCNTTTATCTATCTATCT
ATCTATCTATCNCTATCTATCNCANACCNGGNGAANTNATNTTTGNGAGATTNATGC
AAGNCTGAGAAANACCNAAGAANCTGCTCCCTGTNAAACTNGAGATNCAAGAANCT
GAANAGTATAGNTCCAGTCCNAAGTCTANAGACCTTAGAATTAGGAAAACTGATAC
TATAAATACCAGTGTAAGTCTGAAAGCCTTAAANACCANATAGTGCCATTGAAAGG
GCAGAAGACTGATGTCCCAGTTCAAGCAGGCAAAGTTAGAGAAGCCTTATTTTCTGC
AACATTGTTCTATTCAGACCCTTNANANGATTGACNATGTCCACCCA (SEQ ID NO:80)

Genbank ID: G08001
Description: human STS CHLC.GATA52H04.P16177 clone GATA52H04.
Search for GDB entry

<u>WI-2620:</u>

Database ID: MR1436 (Also known as G03602, D18S890, HHAa12h3, 2620)
Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:
   Left = TCTCCAAGCTATTGATTGGATAA (SEQ ID NO:81)
   Right = TTAAGAGCCAATTTATATAAAAGCAGC (SEQ ID NO:82)
   Product Length = 177
   Review complete sequence:
CCCCTTTTGCCAACGCCATGCTTCACGTAGGGAGCCTGACATGCAGAAAACTCTCCA
AGCTATTGATTGGATAAAGAGCCAGAGCTGACTGAATTCCATTCTTCTTGAGCCTCT
CATTCTGTGTTTCTCGAATTTTTACCAAAGCATCTTGACACACAAATATCTGACTCAA
GGAAAAGGAAAAACAACTGCTTTTTCTCCAGCTGCTTTTATATAAATTGGCTCTTAA
ACTTTCTAAGTTTATTATGGATA (SEQ ID NO:83)

Genbank ID: G03602
Description: WICGR: Random genome wide STSs
Search for GDB entry

<u>WI-4211:</u>

Database ID: MR6638 (Also known as G03617, D18S980, 4211)

Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:
    Left = ATGCTTCAGGATGACGTAATACA (SEQ ID NO:84)
    Right = AAATTCTCGCTGATTGGAGG (SEQ ID NO:85)
    Product Length = 113
    Review complete sequence:
CTAGTACCATAATCCCTTTTGGAATAAACCATCCCACCTTTAGTCAGANCAGATGCT
TCAGGATGACGTAATACATAATAAGCCTACTCAGTTCTACTCTGGCTTTGTATGTCTT
CAAAGTGATATTTTTTAAGTATTACTTGTCCCTCCAATCAGCGAGAATTT (SEQ ID
NO:86)

Genbank ID: G03617
Description: WICGR: Random genome wide STSs
Search for GDB entry

D18S876:

Database ID: GATA-D18S876 (Also known as G09963, CHLC.GATA61E10, D18S876)
Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
    Left = TCAAACTTATAACTGCAGAGAACG (SEQ ID NO:87)
    Right = ATGGTAAACCCTCCCCATTA (SEQ ID NO:88)
    Product Length = 171
    Review complete sequence:
AAGACTGCAATTACATTTGCATCAAACTTATAACTGCAGAGAACGTTGCCCACTATT
TTATACCACACAACAGTATTCTTAGCCAGATTACATCTATCTATCTATCTATCTATCT
ATCTATCTATCTATCTATCTATCTATCATCTATCTAGCTAGCTATCTATCTATAGAAC
TAATGGGGAGGGTTTACCATGTTTGGGTGAACCCAAACATTTTATGGNCAAGGGNTT
GGAAAATTACCCTTATCTACAACTNTTNAACTTGTTTTGGTAGGNGTGNTAATTCCN
TGGGNTTGGAANAACTTTTGNAATTTCCTCNTTGTTTNTNATTNNNNATTNNTNNNC
ATTATTNTGGGGTNTTCNGGGTGGAGGGCTNANTTTGGCCNCCCGGGTCCNNGGNG
CNAGTNGGNNNGGNTNNTNGGGTTTNCTTGGGAANCNTNCCNCCTNCNGGGGNTTC
ANGGGNTTTTTNTTTNNTTG (SEQ ID NO:89)

Genbank ID: G09963
Description: human STS CHLC.GATA61E10.P17745 clone GATA61E10.
Search for GDB entry

GCT3G01:

Database ID: GCT-P10825 (Also known as G09484, CHLC.GCT3G01,
CHLC.GCT3G01.P10825)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
    Left = CTTTGCAATCTTAGTTAATTGGC (SEQ ID NO:90)
    Right = GAACTATGATATGGAGTAACAGCG (SEQ ID NO:23)
    Product Length = 128
    Review complete sequence:
AGATGTTTAACTTTGCAATCTTAGTTAATTGGCAGAAATGAAATTTAGTTTCCACAA
CTTTTATTCGATATTAAAACACCACCACCATCAGCAGCAGCAGCAGCAGCAGCAGC
ATCGCTGTTACTCCATATCATAGTTCAGAGCATTTAAAGNGGTCAAAATATACAACT
AGGCTGACACCNGNATAAGGTTTAATTTTAAACCNGNGGTCTNCCCTCTAAGGNGG
NTTTTTTTTTCTTGNCNTGGCTTCTTTTTCCNTTTGCTTTTGTAAAATATCAAGGNATT
TTTGGGTTNTTCNTGGNANTTNNCNNANTNNTNNTTNNNCNCNCCCCCNTTTGNGG
CGGGGGTCCCCNNNTTGCCCCGGGGTTGNGTGCAGTAGGGGGGGTCNCGGGTNNNGN
AAGTTTNGGGGCCCT (SEQ ID NO:91)

Genbank ID: G09484
Description: human STS CHLC.GCT3G01.P10825 clone GCT3G01.

WI-528:

Database ID: MH232 (Also known as G03589, 528, D18S828)
Source: WICGR: Random genome wide STSs
Chromosome: Chr18

Primers:
    Left = TTCTGCCTTTCCTGACTGTC (SEQ ID NO:92)
    Right = TGTTTCCCATGTCTTGATGA (SEQ ID NO:93)
    Product Length = 211
    Review complete sequence:
CTACTAAGCAAATTCTGCTCAGCCTTCTGCCTTTCCTGACTGTCTTGTTGGCCCTTCC
CACTTTAAGGATGCCTGTTTAAGTAGCCACCTCTAATTAGGAATCTTCCCTTGTTCTT
TCTCAGGAGGCTTAGACACTGTCAGTTTCCTGAAGACAGAAAATAAGCCTGCATTAT
CCTAGTAGTGGATTCAAAACTAATTGTGTCCTGAGTCTTTCAATCATCAAGACATGG
GAAACACTCAACAG (SEQ ID NO:94)

Genbank ID: G03589
Description: WICGR: Random genome wide STSs
Search for GDB entry

25. WI-1783:

Database ID: MR432 (Also known as G03587, _shu_31.Seq, 1783, D18S824)
Source: WICGR: Random genome wide STSs

Chromosome: Chr18

Primers:
    Left = CCAGTAATTAGACATTGACAGGTTC (SEQ ID NO:95)
    Right = TTTTACTAGACAGGCTTGATAAACAA (SEQ ID NO:96)
    Product Length = 305
    Review complete sequence:
CCAGTAATTAGACATTGACAGGTTCCATACTAGTAATGTAGGGAATAGGGCTGCTGC
TTTTTGGGTTTCCTTGAGTATACTTTGTGCTGCATAAATATGGCAATGGATAGTAAAT
AATTTGTATGCAGACCTTTAGTGTCGATTAACCTGTGAATAAGGGAACAACAATCAA
GGACAAAAATCAAAAGACTAATTCTCTATACATTTTGAGCTTTTGTAAAAAAGTAAG
ATTAGCTGAATATATCTGAAAAATTTCTAATCTCCTTTACAATTTTTTAAATTGTTTA
TCAAGCCTGTCTAGTAAAAATAATTCAGTTCGGAATGTGG (SEQ ID NO:97)

Genbank ID: G03587
Description: WICGR: Random genome wide STSs
Search for GDB entry

D18S477:

Database ID: AFM301XF5 (Also known as 301xf5, Z24212, D18S477)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = GGACATCCTTGATTTGCTCATAA (SEQ ID NO:98)
    Right = GATTGACTGAAAACAGGCACAT (SEQ ID NO:99)
    Product Length = 243
    Review complete sequence:
GGACATCCTTGATTTGCTCATAATACACTCATTCCTTTCACCATTGAGTGTGCACATA
TTTCTCTGATTGGAAAGAACTACAGAGGAGGTTTTACNTTTTACTTTCCAGTTTGCTA
TTAAAGAGAGAAAACTAACAGAGNGAAATCAAGCAACTCAAAACAACCTTACACAC
ACACACACACACACACTCACAAAGATATTTGTTCACCATATGTATTGATGTGCC
TGTTTTCAGTCAATCCACAGGAAGGGCTAAGGAGAGTGACATCTGGGCTACATTAA
AAGGACAGTCACATTGCTCAAAGNACTCAAGTTTAGCCCGAGTACAGTAGCT (SEQ
ID NO:100)
Genbank ID: Z24212
Description: H. sapiens (D18S477) DNA segment containing (CA) repeat; clone
Search for GDB entry

D18S979:

Database ID: GATA-P28080 (Also known as G08015, CHLC.GATA92C08,
CHLC.GATA92C08.P28080)

Source: CHLC: genetically mapped polymorphic tetranucleotide repeats
Chromosome: Chr18

Primers:
    Left = AGCTTGCAGATAGCCTGCTA (SEQ ID NO:101)
    Right = TACGGTAGGTAGGTAGATAGATTCG (SEQ ID NO:102)
    Product Length = 155
    Review complete sequence:
CTCTACAGTCTCTNACCTTTGGACTCCAGGACTTTCACCAGCACCCTCAACATTCCCA
CTGGGTTCTCAGGACTTTATAGTTGTACTGAGCCATGCCACTGGATCCTAGGGTCTC
C<u>AGCTTGCAGATAGCCTGCTA</u>TGGGACTTAATCTTTGTAATAAGGTGAGTCAATTCT
GCCAATAAACCTACTTTCATCTCTATCTATCTATCTATCTATCTATCTATCTATCTATA
TCTATCATCTATCTAT<u>CGAATCTATCTACCTACCTACCGTA</u>TTAGTTCTGTCTCTCTGG
AGN (SEQ ID NO:103)

Genbank ID: G08015
Description: human STS CHLC.GATA92C08.P28080 clone GATA92C08.

<u>WI-9340:</u>

Database ID: UTR-05134 (Also known as G06102, D18S1034, 9340, X60221)
Source: WICGR: Primers derived from Genbank sequences
Chromosome: Chr18

Primers:
    Left = TGAGAGAACGAAATCTCTATCGG (SEQ ID NO:104)
    Right = AGGCAGCAAGTTTTTATAAAGGC (SEQ ID NO:105)
    Product Length = 115
    Review complete sequence:
ATGTATCTATCCCAATTGAGTCAGCTAGAAACAGTTGACTGACTAAATGGAAACTAG
TCTATTTGACAAAGTCTTTCTGTGTTGGTGTCTACTGAAGTTATAGTTTACCCTTCCT
AAAAATGAAAAGTTTGTTTCATATAG<u>TGAGAGAACGAAATCTCTATCGG</u>CCAGTCA
GATGTTTCTCATCCTTCTTGCTCTGCCTTTGAGTTGTTCCGTGATCATTCTGAATAAG
CATTT<u>GCCTTTATAAAAACTTGCTGCCT</u>GACTAAAGATTAACAGGTTATAGTTTAAA
TTTGTAATTAATTCTACCATCTTGCAATAAAGTGACAATTGAATG (SEQ ID NO:106)

Genbank ID: G06102
Description: WICGR: Random genome wide STSs
Search for GDB entry

<u>D18S466:</u>

Database ID: AFM094YE5 (Also known as 094ye5, Z23354, D18S466)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = ACACTGTAGCAGAGGCTTGACC (SEQ ID NO:107)
    Right = AGGCCAAGTTATGTGCCACC (SEQ ID NO:108)
    Product Length = 214
    Review complete sequence:
aaatgacactttaaggaggtaacactgtagcagaggcttgaccaccacccagttctcactagcactgaggatgctctattggttgggttaccc
acacacgcatagacatgcacacacacagacacacagacacacacacacacacacacaccagatatagcattccaaaccatcaatatgc
tatgcaatactgcattaacaggtcatgcctgtggtggcacataacttggcctagaaaatactggggacgtctgcattccctttttattatcgaattg
acttacttggcttctgagtttcctcagaagtaatacttcaatacctcttccatttctgccttgancattgtttggggtaccaagtatagct (SEQ
ID NO:109)

Genbank ID: Z23354
Description: H. sapiens (D18S466) DNA segment containing (CA) repeat; clone
Search for GDB entry

D18S1092:

Database ID: AFMA112WE9 (Also known as D18S1092, w5374, a112we9)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = CTCTCAAAGTAAGAGCGATGTTGTA (SEQ ID NO:110)
    Right = CCGAAGTAGAAAATCTTGGCA (SEQ ID NO:111)
    Product Length = 163
    Review complete sequence:
agctctcaaagtaagagcgatgttgtaactgactgagttgttttgtgaanttttgnttttggagtcagtggagcatgttattagatgtaaatttaaac
acacacacacacacacacacacacgagaagtaagtgccaagattttctacttcggcgcctatatttctatatactgattttctgtatttc
ccagacttgaatatagattgtctttctgntttatcatagacaatctcataataanttaggcataataaggtaatgaggnttttctgggcttcttttcat
catccctgcaatttgagtctcntttatagntgaantcttctctgtaataacntcttgttttagct (SEQ ID NO:112)

Search for GDB entry

D18S61:

Database ID: AFM193YF8 (Also known as 193yf8, Z16834, D18S61)
Source: J Weissenbach, Genethon: genetically mapped polymorphic STSs
Chromosome: Chr18

Primers:
    Left = ATTTCTAAGAGGACTCCCAAACT (SEQ ID NO:113)
    Right = ATATTTTGAAACTCAGGAGCAT (SEQ ID NO:114)
    Product Length = 174
    Review complete sequence:

CGTCTTACCAAACCAACATAATATAGCAATGGNAACCAAAA<u>ATTTCTAAGAG</u>
<u>GACTCCCAAAC</u>TACATTCTTCTNCCTGAATTAAATACAGGCATTCAANANAAACANA
CACACACACACACACACACACACACACACACACACGCACACCCTTCAAATCNTA
GCATAAATTCCNCTTATATAAACATAACC<u>ATGCTCCTGAGTTTCAAAATAT</u>TGGGTG
GTTCGAAGTTCGAAGCAACAAATTTCCAGTTAGTGTCTATTANTTGTTGGACAGCT
(SEQ ID NO:115)

Genbank ID: Z16834
Description: H. sapiens (D18S61) DNA segment containing (CA) repeat; clone
Search for GDB entry

Markers (STRs) used in refining the candidate region.

Below the markers are shown that were used in family MAD31 to refine the candidate region.
Most of these markers are already described above and will therefore only be mentioned to by
their name. For the additional markers, the information is given here.

Data was already shown for: D18S68, D18S55, D18S969, D18S1113, D18S483, D18S465,
D18S876, D18S477, D18S979, D18S466 and D18S61.

New data:

<u>D18S51</u>:

Other names: UT574, (D18S379)
Primer sequences:
UT574a   GAGCCATGTTCATGCCACTG (SEQ ID NO:116)
UT574b   CAAACCCGACTACCAGCAAC (SEQ ID NO:117)

DNA-sequence:
       AATTGAGCNCAGGAGTTTAAGACCAGCCTGGGTAACACAGTGAGACCCCTGT
CTCTACAAAAAAATACAAAAATNAGTTGGGCATGGTGGCACGTGCCTGTAGTCTCA
GCTACTTGCAGGGCTGAGGCAGGAGGAGTTCTTGAGCCCAGAAGGTTAAGGCTGCA
GT<u>GAGCCATGTTCATGCCACTG</u>CACTTCACTCTGAGTGACAAATTGAGACCTTGTCT
CAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAANGAAAGAAAGAAA
GTAAGAAAAGAGAGGGAAAGAAAGAGAAANAGNAAANAAATAGTAGCAACTGTT
ATTGTAAGACATCTCCACACACCAGAGAAGTTAATTTTAATTTTAACATGTTAAGAA
CAGAGAGAAGCCAACATGTCCACCTTAGGCTGACGGTTTGTTTATTTGTGTT<u>GTTGC</u>
<u>TGGTAGTCGGGTTTG</u>TTATTTTTAAAGTAGCTTATCCAATACTTCATTAACAATTTCA
GTAAGTTATTTCATCTTTCAACATAAATACGNACAAGGATTTCTTCTGGTCAAGACC
AAACTAATATTAGTCCATAGTAGGAGCTAATACTATCACATTTACTAAGTATTCTAT
TTGCAATTTGACTGTAGCCCATAGCCTTTTGTCGGCTAAAGTGAGCTTAATGCTGATC
GACTCTAGAG (SEQ ID NO:118)

GENBANK ID: L18333

<u>D18S346.</u>

Other name: UT575

Primer Pairs:

Primer A: TGGAGGTTGCAATGAGCTG (SEQ ID NO:119)
Primer B: CATGCACACCTAATTGGCG (SEQ ID NO:120)

DNA sequence:
ACGAGGACAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAACCCCGTTTNTACTA
AAANTACAAAANTTGGTCGGGAGGCTGGGGCAGGNGACATGCTTGACCCCAGGAGG
<u>TGGAGGTTGCAATGAGCTG</u>AGATTGCACCACTGCACTNCAGCNTGG. (SEQ ID
NO:121).....AAGAAAGAGAAAGGANAGNNAGGNAGNNANNAAACTACATNTGAAGTC
AACACTAGTATTGGTGGGAGAGGAATTTTATGCTGCATTCCCCNACAACCACTAGAT
A<u>CGCCAATTAGGTGTGCAT</u>GGTCCATGCTAT (SEQ ID NO:122)

GenBank ID: L26588

<u>D18S817.</u>

Other name: UT6365

Primer Pairs:

Primer A: GCAAAGCAGAAGTGAGCATG (SEQ ID NO:123)
Primer B: TAGGACTACAGGCGTGTGC (SEQ ID NO:124)

DNA Sequence:

CATATGGGTCCACAAGCAACCTCAGTCCTTGTCTCTTCAGAAGAAAGAATTCTACTG
AGGGNCATAAGGCAGAAGGAGAGACCTAGGCAAGTT<u>GCAAAGCAGAAGTGAGCAT</u>
<u>G</u>TATTAAAAAGCTTTAGAACAGTAAGGAAAGGAAGAAAAGAAAAGAAGGAAAGTT
CAACTTGGAAGAGGGCCAAGCCGGCAACTTGGCAGAAGGATTGCTTGAGCCCAGGA
GTTAAGACCAGTCTGGGCAATATAGTGAGACTCCATCTCTGCATACATACATACATA
CATACATACATACATACATACATACATATTGCAGGGTATGATG<u>GCACACGCCTGTAG</u>
<u>TCC</u>TAGCTACTCTGGAGGTTGAGATGGGAGGGTCACTGAGCCTGGGAANTTGAGGC
TGCNNTGAGCCATGATC (SEQ ID NO:125)

GenBank ID: L30552

Characterisation of YACs.

8 YACs were selected covering the candidate region and flanking the gap. These YACs were
further characterised by determining the end-sequences by the Inverse-PCR protocol.

Selected YACs: 961_h_9, 942_c_3, 766_f_12, 731_c_7, 907_e_1, 752_g_8, 717_d_3, 745_d_2

New STSs based on end-sequences (unless indicated otherwise, the STSs were tested on a monochromosomal mapping pannel for identifying chimaerism of the YAC; if the STS revealed a hit not on chromosome 18q -chimaeric YAC- then it is indicated in the text below):

SV32L.

Derived from YAC 745_d_2 left arm end-sequence.

Primer A: GTTATTACAATGTCACCCTCATT (SEQ ID NO:126)
Primer B: ACATCTGTAAGAGCTTCACAAACA (SEQ ID NO:127)

DNA-sequence:

ATTCCTTNGTTATTACAATGTCACCCTCATTTAAAAAGTGGAAAGATAAAGAGGAAG
CAATCTATTTTTTTCCTTTTTTTTCTGATAGCACTTGTTTGTGAAGCTCTTACAGATGTT
CTTAAGTAAAATCAACTCCTCCATTTTTTTTGTAGCAACTACACATATTTATCAATAA
TAGTTCACAAATACATTTTCAAATT (SEQ ID NO:128)

Amplified sequence length: 107 basepairs (bp)

This STS has no clear hit on the monochromosomal mapping pannel.

SV32R.

Derived from YAC 745_d_2 right arm end-sequence.

Primer A: ACGTTTCTCAATTGTTTAGTC (SEQ ID NO:129)
Primer B: TGTCTTGGCATTATTTTTAC (SEQ ID NO:130)

DNA sequence:

AGACAATGGGAGAAATTGCACTGCCCTGAGTCAGAAATCAGATCTGTTGCCATACA
GCTGCCGTTATGTGATCATTTGCAAGTCAACGTTTCTCAATTGTTTAGTCATTTGTAA
GACAAAAAGACTGGTTGGATTTCAGAGAATTTGGAATCCTCCTTCAGGTTTAACAAG
CAATAAATGATACTCTTCAGTGTAAAAATAATGCCAAGACATNATTTGACTTTAAAT
TAAATCCAAACAAGATATC (SEQ ID NO:131)

Amplified sequence length: 127 bp

This STS has no clear hit on the monochromosomal mapping pannel.

SV11L.

Derived from YAC 766_f_12 left arm end-sequence.

Primer A: CTATGCTCTGATCTTTGTTACTTT (SEQ ID NO:132)
Primer B: ATTAACGGGAAAGAATGGTAT (SEQ ID NO:133)

DNA sequence:

GTCTTTATTTCATATAACTATGCTCTGATCTTTGTTACTTTCTCCTTTTAACTCAGTTT
AAGCTTTATTCTTATTTTCCAGCTGCTGAAGGTATATAGTTAGGTTGTTTATTGGATA
CCATTCTTTCCCGTTAATGTCAGTGGTTACTGCTATCAATGTAGCAGTTA (SEQ ID
NO:1)

Amplified sequence length: 118 bp

This STS has a hit with chromosome 18 and must ba located between CHLC.GATA-p6051 and
D18S968.

SV11R.

Derived from YAC 766_f_12 right arm end-sequence.

Primer A: AAGGTATATTATTTGTGTCG (SEQ ID NO:134)
Primer B: AAACTTTTCTTAACCTCATA (SEQ ID NO:135)

DNA sequence:

ATAAGGTATATTATTTGTGTCGTGAGTTAAGAAATCATTAATAACTATTTTCAGAAT
GACAAATGTCATTATATGTTGTAAAAAGATAAATACGTGAAATTATGAGGTTAAG
AAAAGTTTA (SEQ ID NO:2)

Amplified sequence length: 119 bp.

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01.

SV34L.

Derived from YAC 717_d_3 left arm end-sequence.

Primer A: TCTACACATATGGGAAAGCAGGAA (SEQ ID NO:136)
Primer B: GCTGGTGGTTTTGGAGGTAGG (SEQ ID NO:137)
DNA sequence:

ACATAAAATGTCGCTCAAAAACAATTATGTGTG<u>TCTACACATATGGGAAAGCAGGA</u>
<u>A</u>ACAAATTTGTTTACAACATACATTACTTTTGTTTTTTAGGCAAGATAAAATNT<u>CCTA</u>
<u>CCTCCAAAACCACCAGC</u>ACNGTCCGCAATAACTATACATC (SEQ ID NO:3)

Amplified sequence length: 98 bp

This STS has a hit with chromosome 18.

SV34R.

Derived from YAC 717_d_3 right arm end-sequence.

Primer A: ATAAGAGACCAGAATGTGATA (SEQ ID NO:138)
Primer B: TCTTTGGAGGAGGGTAGTC (SEQ ID NO:139)

DNA-sequence:

AATATCATTCTTCACCCACGTTATAC<u>ATAAGAGACCAGAATGTGATA</u>TTGTCATCTC
ACATGGAAAAATCTGCTGTGATCAGTTCCTGAAGCTTGCTGTGATCCTCCCTTAGGA
AAGTAGAAAAATCTTTTTGAAACACTTTATTCTACAATCAATGAAAATTAGGTGAAG
CTACAGAAGCCAGAAATTACTCTAAGATTAGACAATTATTTAAGANGACCAATTGTC
TTTGGTCTTCTTCTGAAGGGTCT<u>GACTACCCTCCTCCAAAGA</u>ATTCACTGGCCGTCGT
TTTACAACGTCNTGA (SEQ ID NO:4)

Amplified sequence length: 244 bp

This STS has a hit with chromosome 1, therefore YAC 717_d_3 is chimaeric

SV25L.

Derived from YAC 731_c_7 left arm end-sequence.

Primer A: AAATCTCTTAAGCTCATGCTAGTG (SEQ ID NO:140)
Primer B: CCTGCCTACCAGCCTGTC (SEQ ID NO:141)

DNA sequence:

AGTGGAGAGATAGAAAGAGAGGAAGATTTTTTTTTT<u>AAATCTCTTAAGCTCATGCT</u>
<u>AGTG</u>TAGGTGCTGGCAGGTCTGAACACTCTGTAG<u>GACAGGCTGGTAGGCAGG</u>AA
(SEQ ID NO:142)

Amplified sequence length: 72 bp

This STS has no clear hits on the monochromosomal mapping pannel.

SV25R.

Derived from YAC 731_c_7 right arm end-sequence.

Primer A: TGGGGTGCGCTGTGTTGT (SEQ ID NO:143)
Primer B: GAGATTTCATGCATTCCTGTAAGA (SEQ ID NO:144)

DNA-sequence:

GGAGGGTGTTNTCACANAAGTCTGGGGTGCGCTGTGTTGTTCATTGTAAAAACCCTT
TGGANCATCTGGGAATGTGCTGCCCCACATGTCCAGGTAACGTTCTCAGGAAGGGG
AGGCTGGAAATCTCTGTGTGTTCTTACAGGAATGCATGAAATCTCCCANCCCCTCTT
GTTGGAAATTTCCCTCACTTT (SEQ ID NO:5)

Amplified sequence length: 136 bp

This STS has a hit with chromosome 7; therefore YAC 731_c_7 is chimaeric

SV31L.

Derived from YAC 752_g_8 left arm end-sequence.

Primer A: GAGGCACAGCTTACCAGTTCA (SEQ ID NO:145)
Primer B: ATTCATTTTCTCATTTTATCC (SEQ ID NO:146)

DNA-sequence:

CTTCTCNATGANTGGACAAATGTCATTGGGTCAGCATGAGGCACAGCTTACCAGTTC
AGATTCCAGTAGCTGAGGAACAAATCTTAACTCCAAAAATAAGTAATTGCGTCACTT
TGGAGGAATTATTTGACCTTTTCATAACTTTGACATCACAACAATGAGGGTGAAGTT
AGTAAAATAAATGATTATTATGAGGATAAAATGAGAAAATGAATTNAGTGCTTAAG
ACAATGCTTGGTAACTAGTTAANCCG (SEQ ID NO:6)

Amplified sequence length: 178 bp

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01.

SV31R.

Derived from YAC 752_g_8 right arm end-sequence.

Primer A: CAAGATTATGCCTCAACT (SEQ ID NO:147)
Primer B: TAAGCTCATAATCTCTGGA (SEQ ID NO:148)

631568.1

DNA sequence:

AAACTTTAACCAATTTAAACTCCCTAACAGTTCTATAAAATAAGCAAGATTATGCCT
CAACTTTATGGATAAAGAAATGGAGGCATTAAGAGATAACTAACTTGCCCAAGGCC
ACACAAGTGACTGAGTAAGAATTGCAAAGCCAATGAGTCTGGCTCCAGAGATTATG
AGCTTAATCACCACACTGTGCCACCTCCTGTGTTCCTGG (SEQ ID NO:149)

Amplified sequence length: 131 bp

This STS has no clear hits on the monochromosomal mapping pannel and gives no information concerning the chimaerity of the YAC.

SV10L.

Derived from YAC 942_c_3 left arm end-sequence.

Primer A: TCACTTGGTTGGTTAACATTACT (SEQ ID NO:150)
Primer B: TAGAAAAACAGTTGCATTTGATAT (SEQ ID NO:151)

DNA-sequence:

GGTNTTTCACTTGGTTGGTTAACATTACTTCTAAGTTTTTTATTGTTTTTTATGCTATT
GCTAATGGGATTGCTTTCTTAATTTATTTTTTCCAATAGCTTGTTGTTAGTTTATATCA
AATGCAACTGTTTTTCTATGCAAATTATGTTTCCT (SEQ ID NO:7)

Amplified sequence length: 130 bp

This STS has a hit with chromosome 18 and must be located between CHLC.GATA-p6051 and D18S968

SV10R.

Derived from YAC 942_c_3 right arm end-sequence.

Primer A: AACCCAAGGGAGCACAACTG (SEQ ID NO:152)
Primer B: GGCAATAGGCTTTCCAACAT (SEQ ID NO:153)

DNA sequence:
TTGGTGGTGCCCTAGGTTTGGCAATTATAAATAAAGCTGCTACAAACATTCATGTGC
AGGTCTCCGTGTGGACATAATTTTCCAGTTCATTTGGGTAAAACCCAAGGGAGCACA
ACTGTTGGATCCTATNATAAAAATATNTCTCGTTTCATTTAAAAAACCTGGGAAACT
ATCTNCCCACAGTGGCTGTCCCTTTTTGTATCCCCACCAACAATGTTGGAAAGCCTAT
TGCCANCAT (SEQ ID NO:8)

Amplified sequence length: 135 bp

This STS has a hit with chromosome 18 and must be located between D18S876 and GCT3G01

SV6L.

Derived from YAC 961_h_9 left arm end-sequence.

No primer was made, because this sequence is identical to a known STR marker D18S42, which is indeed mapped to this region.

Primer A:
Primer B:

DNA sequence:

CATGNCTCACAGTGTTCTGAGGCTGCTCTGGACATGCAATCTTGCATGCTTTTGTCAT
GACAGGTCTTAAANAGTTTATCAGCTTNCTCAAATAGCTGAATGACANAACACTGG
ATTTTTGTTCAAATANCCTATCAACTTGGCNTCTGTGTTGCGGTTGTCACTTGGTAAC
AAAATAAGTC (SEQ ID NO:9)

Amplified sequence length:

SV6L recognises D18S42 which must be therefore located between WI-7336 and WI-8145

SV6R.

Derived from YAC 961_h_9 right arm end-sequence.

Primer A: TTGTGGAATGGCTAAGT (SEQ ID NO:154)
Primer B: GAAAGTATCAAGGCAGTG (SEQ ID NO:155)

DNA sequence:

TAATTGACAAATAAAAATTGTATATTTTNCATATTTAACATGTTATGCTAACATATAT
ATGGATTGTGGAATGGCTAAGTCAGAAATTCTTTTACATTCATATTTCCATATTATTT
ACTTTNNGCTTTAAAAAATATGTAAATGANAATACTTATTTTTTTCAGTGTCACTGCC
TTGATACTTTCACATTTNNGTTACATATTATTTCCCTTNCATCTAACAAATATATATT
GAGTTTCTATAATGTGTCTGACACTGA (SEQ ID NO:10)

Amplified sequence length: 122 bp

SV6R amplifies a segment on chromosome 18. This segment must be located between WI-2620 and WI-4211

631568.1

SV26L.

Derived from YAC 907_e_1 left arm end-sequence.

Primer A: TATTTGGTTTGTTTGCTGAGGT (SEQ ID NO:156)
Primer B: CAAGAAGGATGGATACAAACAAG (SEQ ID NO:157)

DNA sequence:

TGGTCACTGGTGCCTTATTTGGTTTGTTTGCTGAGGTCATATTTCCTGTGGCCTTCAT
GCTTGATTTGTTGGAGTCTAGCCATGTAAAANTCTGTTGGAGTCTAGGCATTTAAAA
AATAGGTATTTATTGTAATCTTTGCCATTTGCTTGTTTGTATCCATCCTTCTTGGGAA
GGCTTTACAGGCATTCAAAAGG (SEQ ID NO:11)

Amplified sequence length: 154 bp

This STS has a hit with chromosome 13; therefore YAC 907_e_1 is chimaeric.

SV26R.

Derived from YAC 907_e_1 right arm end-sequence.

Primer A: CGCTATGCATGGATTTA (SEQ ID NO:158)
Primer B: GCTGAATTTAGGATGTAA (SEQ ID NO:159)

DNA sequence:

CGCTATGCATGGATTTAAACTGAGTGTAGTGCACTCACTATGTTGCAGTCTCTTATTC
TAGGTTCCTAATATTTACATCCTAAATTCAGCT (SEQ ID NO:160)

Amplified sequence length: 90 bp

no clear hits on monochromosomal mapping pannel: no information concerning chaemerity at
this side of the YAC

Page 64, line 5 through line 19:

A 4.5kb ECORI/SalI fragment of pBLC8.1 (Lewis *et al*, 1992) carrying a lysine-2 and a
telomere sequence was directionally cloned into GEM3zf(-) digested with ECORI/SalI.

631568.1